In the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

1-21. (cancelled)

22. (currently amended) A method for designing proteins comprising:

generating backbone protein configurations of fixed length using a set of dihedral angle pairs;

assigning a sphere of fixed radius or another space-filling generic side chain to each position where an amino acid residue would be in the generated configurations;

eliminating self-intersecting configurations;

evaluating the surface exposure of each sphere or generic side chain in each remaining configuration;

normalizing the total surface exposure of each remaining configuration;

generating ~~a random set of~~ sequences of hydrophobicities ~~with uniform weight on the space of allowed sequences for each remaining configuration~~ having the same length as the number of spheres or generic side chains in the remaining generated configurations;

determining, for each ~~randomly generated~~ sequence of hydrophobicities, which of the remaining configurations is the ground state;

recording the ground-state configuration for each sequence; ~~wherein desirable configurations are those containing the most sequences with that configuration as their ground state,~~

identifying as highly designable those configurations which are ground states of the largest number of sequences; and

~~synthesizing~~ selecting sequences of amino acids ~~for the desirable~~ designed to adopt one of the highly designable configurations.

23. (original) A method for designing proteins as in claim 22 wherein:

one set of dihedral angle pairs corresponds to an alpha helix and one set of dihedral angles corresponds to a beta strand.

24. (original) A method for designing proteins as in claim 22 wherein:

two sets of dihedral angles correspond to an alpha helix and one set of dihedral angle pairs corresponds to a beta strand.

25. (original) A method for designing proteins as in claim 24 wherein:

additional dihedral angle pairs fall within regions of high frequency in a Ramachandran plot.

26. (currently amended) A method for designing proteins as in claim ~~25~~ 22 wherein:

the probability of choosing a particular pair of dihedral angles depends on the ~~preceeding~~ preceding pairs of dihedral angles along the backbone.

27. (cancelled)

28. (previously presented) A method for designing proteins as in claim 22 further comprising:

eliminating non-compact configurations.

29. (currently amended) A method for designing proteins as in claim 28 further comprising:

clustering configurations which are sufficiently similar in the three dimensional ~~trajectory followed by~~ trajectories of their backbones and ~~treating~~ considering all configurations within such a cluster ~~as~~ to be variants of a single ~~configuration, and;~~ configuration;

summing, for all configurations in a cluster, the number of sequences with that configuration as their ground state; and ~~such that the sum is considered the designability of the cluster~~ identifying as highly designable those clusters of configurations with the largest sum of associated sequences.

30. (currently amended) A method for designing proteins ~~as in claim 29 further~~ comprising:

generating backbone protein configurations of fixed length using a set of dihedral angle pairs;

assigning a sphere of fixed radius or another space-filling generic side chain to each position where an amino acid residue would be in the generated configurations;

eliminating self-intersecting configurations;

evaluating the surface exposure of each sphere or generic side chain in each remaining configuration;

normalizing the total surface exposure of each remaining configuration;

recording the Variance of each configuration remaining after elimination of self-intersecting configurations;~~,~~

ranking the configurations from highest Variance to ~~lowest, and~~ lowest;

~~designing proteins starting with the~~ identifying as highly designable those configurations having the highest Variance; and

selecting sequences of amino acids designed to adopt one of the highly designable configurations.

31. (original) A method for designing proteins as in claim 22 wherein:

the set of dihedral angles is a set of strings of dihedral angles.

32. (original) A method for designing proteins as in claim 31 wherein:

the strings of angles are weighted according to their frequency of appearance in natural proteins and infrequent strings are eliminated.

33. (currently amended) A method for designing proteins as in claim 22 wherein:

normalizing is accomplished by dividing the surface exposure of each ~~amino acid in~~ sphere or generic side chain assigned to a given configuration by the total surface exposure of that configuration.

34. (cancelled)

35. (original) A method for designing proteins as in claim 22 further comprising:

eliminating non-compact configurations after self-intersecting configurations are eliminated.

36. (currently amended) A method for designing proteins as in claim 35 further comprising:

clustering configurations which are sufficiently similar in the three dimensional ~~trajectory followed by~~ trajectories of their backbones and ~~treating~~ considering all configurations within a cluster ~~as~~ to be variants of a single ~~configuration, and;~~ configuration;

summing, for all configurations in a cluster, the number of sequences with that configuration as their

ground state; and ~~such that the sum is considered the designability of the cluster~~ identifying as highly designable those clusters of configurations with the largest sum of associated sequences.

37. (original) A method for designing proteins as in claim 22 further comprising:

eliminating all configurations that are not favorable for forming hydrogen bonds after eliminating non-compact configurations.

38. (currently amended) A method for designing proteins as in claim 22 further comprising:

clustering configurations which are sufficiently similar in the three dimensional ~~trajectory~~ ~~followed by~~ trajectories of their backbones and ~~treating~~ considering all configurations within a cluster ~~as~~ to be variants of a single ~~configuration, and;~~ configuration;

summing, for all configurations in a cluster, the number of sequences with that configuration as their ground state; and ~~such that~~ ~~the sum is considered the designability of the cluster~~ identifying as highly designable those clusters of configurations with the largest sum of associated sequences.

39. (original) A method for designing proteins as in claim 38 wherein:

clustering is accomplished by totaling the root-mean-square distance between every pair of configurations and defining a configuration as a member of a cluster if it lies within a root-mean-square distance λ of any member of the cluster.

40. (original) A method for designing proteins as in claim 39 wherein:

λ is 0.4 Angstroms per amino acid.

41-57. (cancelled)